REMARKS

Claims 13, 15-17, 21, 25-29, and 33-40 are now pending. Claims 13-17, 21, 25-29, and 33-37 have been rejected. Claim 14 has been canceled by this response. New claims 38-40 have been added. Independent claim 13 has been amended by this response. Amendment of claim 13 and cancellation of claim 14 are made without prejudice to subsequent presentation of these claims in a continuing or in a related application.

The Applicants are grateful to the Examiner for the courtesy of a telephonic interview extended to the Applicants' undersigned representative, Anna Gavrilova, on January 7, 2008. During the interview, the Applicants' representative illustrated the claimed methods while making reference to an example shown in Figure 2, and to pertinent portions of the specification. The Examiner has indicated that the method as described at page 15, lines 7-16 of the specification may be patentable over the references of record. The Examiner has acknowledged that the references of record do not describe screening peptoid libraries with the use of arrays of physically separated compartments, as described at page 15, lines 7-16 and in Figure 2. The Applicants are grateful to the Examiner for suggesting an avenue for claim amendments. The Applicants have herein amended the independent claim 13 to recite the use of arrays of physically separated compartments in peptoid library screening. The Applicants have also introduced new claims 38-40, reciting library screening method as described at page 15, lines 7-16.

While Applicants believe that previously presented claim 13 is patentable over references of record, in order to expedite prosecution, the Applicants have herein amended claim 13 to recite the use of arrays of separated compartments.

The amended claim 13 now recites that operations (i) – (iii) of the claimed method make use of an array of physically separated compartments. Support for this amendment is found, for example in Figure 2, which illustrates screening of a peptoid library on a multi-well plate. This amendment is also supported in the specification at page 15, lines 7-16.

The new independent claim 38 recites a method of identifying peptoids which are effective in transfecting a cell with an oligonucleotide. New claim 38 recites:

(i) providing a plurality of different-sequence peptoids in separated compartments, wherein the sequences of individual peptoids are unidentified;

(ii) forming a peptoid-oligonucleotide mixture in at least one of these compartments, wherein said oligonucleotide is between about 10 and 50 nucleotides in length;

(iii) contacting the mixture with a cell;

(iv) determining the degree of transfection of the cell by the oligonucleotide;

(v) after the degree of transfection is determined, determining the identity of the peptoid.

This claim is supported at page 15, lines 7-16. Support for dependent claims 39-40 is also found at page 15, lines 7-16 and in Figure 2.

Rejection based on 35 USC 103(a)

Claims 13-17, 21 and 25-29, 33-34 and 36-37 were rejected under 35 USC 103(a) as being unpatentable over Liotta (USP 6,153,596) in view of Murphy (PNAS) and Furka et al. (Int. J. Peptide Protein Res. 37, 1991, 487-493).

The Applicants have herein amended the independent claim 13 to recite the use of arrays of physically separated compartments for screening a library of peptoids for oligonucleotide transfection. As was acknowledged by the Examiner, the references of record, alone or in combination, do not teach screening peptoids for oligonucleotide transfection with the use of arrays of physically separated compartments.

The Applicants further submit that neither Liotta nor Murphy teach or suggest identifying peptoid sequences *after* transfection has taken place. Rather, both Liotta and Murphy know the chemical identity of each peptoid before transfection. For example, Murphy synthesizes 24 compounds of known sequences (Table 1, p.1519) and subsequently screens them for transfection of plasmid DNA. While some of these 24 compounds are found to be efficient transfecting agents, others do not substantially transfect. One of skill in the art will glean from Murphy's article that in Murphy's method all 24 compounds were identified prior to transfection. In addition, it can be seen that peptoid sequence identification methods are described under the same heading as peptoid synthesis (p.1518, second paragraph), indicating that peptoid identification takes place immediately after peptoids have been synthesized and not after they have been screened for transfection. The Applicants respectfully submit that Murphy contains neither explicit nor inherent teaching for a method involving identification of peptoid sequences after screening for transfection has taken place.

In addition, as was acknowledged by the Examiner, Murphy describes transfection of plasmid DNA and is not concerned with transfection of oligonucleotides at all.

With respect to Liotta, the Applicants reiterate that Liotta does not teach or suggest screening a library of peptoids having unidentified sequences. In all examples provided by Liotta, a peptide of a pre-determined sequence is used for transfection. In fact, no specific and detailed teaching for library screening is provided by Liotta at all. Also, the Applicants bring to Examiner's attention that Liotta does not explicitly teach peptoids of formulas I and II. In his disclosure, Liotta describes a large variety of compounds which include both peptides and peptoids. The Applicants submit that formulas I and II would not be clearly envisaged by one of skill in the art, presented with Liotta. Taking into account Liotta's general teaching of the advantages and desirability of matching positive and negative charges between the transfecting agent and the oligonucleotide to be transfected, the Applicants submit that Liotta's disclosure taken as a whole (even in combination with Murphy and Furka) would not direct one of skill in the art to the method of claim 13.

With respect to Furka, this reference provides background information on mix-and-split method for synthesizing libraries. The reference does not mention peptoid libraries or oligonucleotide transfection at all. At most, this reference suggests to explore the entire field of combinatorial chemistry, and to identify the systems for which mix-and-split protocol could be applicable. No reasonable expectation of success for screening peptoid libraries for transfection with the Furka's method is provided by the combination of the three references.

For at least these reasons, the Applicants respectfully submit that the method claimed in claim 13 is not an obvious variation of Liotta's, Murphy's and Furka's methods, and that the combination of these references' teachings do not render the present claims obvious. Withdrawal of the 103(a) rejection for claim 13 and its dependent claims 14-17, 21 and 25-29, 33-34, and 36-37 is respectfully requested.

Allowance for independent claim 38 and for its dependent claims 39-40 is also respectfully requested.

CONCLUSION

In light of the foregoing remarks, Applicants respectfully submit that all pending claims are in condition for allowance. Thus, Applicants respectfully request a Notice of Allowance from the Examiner. Should any unresolved issues remain, the Examiner is encouraged to contact the undersigned at the telephone number (510) 663 1100.

If any additional fees not submitted with this filing are due in connection with the filing of this Response, the Commissioner is hereby authorized to charge such fees to Deposit Account 500388 (Order No. CHIRP053).

Respectfully submitted,
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